

The above protocols are used to develop primers from Sequence id GM\_M02\_A2\_B07\_MR\_MR containing the following nucleotide composition (SEQ ID NO: 36936):

AGGCGTTTTNCCTTGATACCTTCGNAGGTCCANCCTTTNCTTGCTGTATCGA  
CTCATTAACACCAAGCTCGGTGAGCACTCTGAAGATTATGACAACCTTTCGNTG  
ATCTTTTTTGTTCATCGATATTNTAGNAGAGACCAATCTTTCTTCTTCAAATGTCTG  
CTCATGATATTTATTGTAATTATCTTCAATGTATGTCCAAAAAGTTAACCTTTT  
TTGGACCCCCACAATAGAAATCTTTGAAATATTTAGCCATGTGTTGGCAAGCC  
ATTCATATTTCTTTGCGGAGAAACATGATCTATTGTGTCTTTTCGGATGCTTCTT  
CTATGTtcttcttcttcttcttcttcttcttcttcttCATTGACCACAATATTATCCAACTCAACTTA  
GGTGCAAAATGGTGGAATTTGAGACTTTGACGCANAGTCAGATGGTGCGTCA  
TGCTCTTTCATTACATTGGACATCATNTACTACCCTTTGAAGACCCTCGATCC  
ATGGAAGGGTTAATTGGTG

This sequence contains CTT dinucleotide repeats with a repeat unit of 11. Using the Primer 3 program, two primers are selected: SER157F GTGTCTTTTCGGATGCTTCTTCT (SEQ ID NO: 36937) and SER157R CACCATTTTGCACCTAAGTTGA (SEQ ID NO: 36938). When these two primers are used to amplify genomic DNAs from eight different varieties, Minsoy, Noir, PIC, HS-1, A3244, H6686, A0868 and H5088, three alleles are detected. Sizes of these alleles ranged from 80 to 110 base pairs. The size variation in the PCR products result from repeat numbers in different varieties.

## IN THE CLAIMS

Please **cancel** non-elected claims 17 and 18, without prejudice to or disclaimer of the subject matter contained therein.

Please **amend** the claims as follows:

1. (Twice amended) A substantially purified nucleic acid molecule, said nucleic acid molecule capable of specifically hybridizing, under conditions of 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, to